

RAW SEQUENCE LISTING

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Application Serial Number: 10/551,105A
Source: 1 FWD
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RAW SEQUENCE LISTING

DATE: 02/20/2007

PATENT APPLICATION: US/10/551,105A

TIME: 11:21:27

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\10551105a_efs\Sequence_Listings_CHM003_ST25.txt

Output Set: N:\CRF4\02202007\J551105A.raw

3 <110> APPLICANT: Whitsett, Jeffrey A
 5 <120> TITLE OF INVENTION: USE OF FGF-18 PROTEIN, TARGET PROTEINS AND THEIR RESPECTIVE
 6 ENCODING NUCLEOTIDE SEQUENCES TO INDUCE CARTILAGE FORMATION
 8 <130> FILE REFERENCE: CHM-003
 10 <140> CURRENT APPLICATION NUMBER: 10/551,105A
 11 <141> CURRENT FILING DATE: 2005-09-26
 13 <150> PRIOR APPLICATION NUMBER: US 60/458,224
 14 <151> PRIOR FILING DATE: 2003-03-27
 16 <150> PRIOR APPLICATION NUMBER: PCT/US04/09264
 17 <151> PRIOR FILING DATE: 2004-03-26
 19 <160> NUMBER OF SEQ ID NOS: 14
 21 <170> SOFTWARE: PatentIn version 3.4
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 624
 25 <212> TYPE: DNA
 26 <213> ORGANISM: House Mouse
 28 <400> SEQUENCE: 1
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 31 caggttcagg tggtggcagc cgaggagaat gtggacttcc gcatccacgt ggagaaccag 120
 33 acgcgggctc gagatgatgt gagtcggaag cagctgcgct tgtaccagct ctatagcagg 180
 35 accagtggga agcacattca agttctgggc cgtaggatca gtgcccgtgg cgaggacggg 240
 37 gacaagtatg cccagctcct agtggagaca gataccttcg ggagtcaagt ccggatcaag 300
 39 ggcaaggaga cagaattcta cctgtgtatg aaccgaaaag gcaagctcgt ggggaagcct 360
 41 gatggtacta gcaaggagtg cgtgttcatt gagaaggttc tggaaaacaa ctacacggcc 420
 43 ctgatgtctg ccaagtactc tggttggtat gtgggcttca ccaagaaggg gcggcctcgc 480
 45 aagggtccca agaccgcga gaaccagcaa gatgtacact tcatgaagcg ttaccccaag 540
 47 ggacaggccg agctgcagaa gcccttcaaa tacaccacag tcaccaagcg atcccggcgg 600
 49 atccgccccca ctcaccccg ctag 624
 52 <210> SEQ ID NO: 2
 53 <211> LENGTH: 207
 54 <212> TYPE: PRT
 55 <213> ORGANISM: House Mouse
 57 <400> SEQUENCE: 2
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 60 1 5 10 15
 63 Leu Leu Cys Phe Gln Val Gln Val Leu Ala Ala Glu Glu Asn Val Asp
 64 20 25 30
 67 Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
 68 35 40 45
 71 Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
 72 50 55 60
 75 His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
 76 65 70 75 80

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79 Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
80                               85                               90                               95
83 Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
84                               100                              105                              110
87 Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
88                               115                              120                              125
91 Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
92                               130                              135                              140
95 Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
96 145                               150                              155                              160
99 Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
100                               165                              170                              175
103 Arg Tyr Pro Lys Gly Gln Ala Glu Leu Gln Lys Pro Phe Lys Tyr Thr
104                               180                              185                              190
107 Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Gly
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111 <210> SEQ ID NO: 3

112 <211> LENGTH: 1406

113 <212> TYPE: DNA

114 <213> ORGANISM: Human

116 <400> SEQUENCE: 3

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119 gcagctccgc gcccgggccg gagagcgcaa ctcggtctcc agaccgccc cgcatgctgt      120
121 ccccggaactg agccgggcag ccagcctccc acggacgccc ggacggccgg ccggccagca      180
123 gtgagcgcagc ttccccgcac cggccaggcg cctcctgcac agcggctgcc gccccgcagc      240
125 ccctgcgcca gcccggaggg cgcagcgctc gggaggagcc gcgcggggcg ctgatgccgc      300
127 agggcgcgcc gcggagcgcc ccggagcagc agagtctgca gcagcagcag ccggcgagga      360
129 gggagcagca gcagcgggcg cggcgggcgg ggcggcgggc gaggcgccc gtcccggccg      420
131 cgcggagcgg acatgtgcag gctgggctag gagccgccc ctccctccc cccagcgatg      480
133 tattcagcgc cctccgcctg cacttgccct tgtttacact tcctgctgct gtgcttccag      540
135 gtacaggtgc tggttgccga ggagaacgtg gacttccgca tccacgtgga gaaccagacg      600
137 cgggctcggg acgatgtgag ccgtaagcag ctgcggtctg accagctcta cagccggacc      660
139 agtgggaaac acatccaggt cctgggcccg aggatcagtg cccgcggcga ggatggggac      720
141 aagtatgccc agctcctagt ggagacagac accttcggta gtcaagtccg gatcaagggc      780
143 aaggagacgg aattctacct gtgcatgaac cgcaaaggca agctcgtggg gaagcccgat      840
145 ggcaccagca aggagtgtgt gttcatcgag aagggttctg agaacaacta cacggccctg      900
147 atgtcggcta agtactccgg ctggtacgtg ggcttcacca agaagggcg gccgcggaag      960
149 ggcccccaaga cccgggagaa ccagcaggac gtgcatttca tgaagcgcta cccaagggg      1020
151 cagccggagc ttcagaagcc cttcaagtac acgacggtga ccaagaggtc ccgtcggatc      1080
153 cggcccacac accctgccta ggccacccc cgcgggccct caggtcgccc tggccacact      1140
155 cacactccca gaaaactgca tcagaggaat atttttacat gaaaaataag gattttattg      1200
157 ttgacttgaa acccccgatg acaaaagact cacgcaaagg gactgtagtc aaccacagg      1260
159 tgcttgtctc tctctaggaa cagacaactc taaactcgtc cccagaggag gacttgaatg      1320
161 aggaaccaa cactttgaga aaccaaagtc ctttttccca aaggttctga aaggaaaaaa      1380
163 aaaaaaaaaa aaaaaaaaaa aaaaaa

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166 <210> SEQ ID NO: 4

167 <211> LENGTH: 208

168 <212> TYPE: PRT

169 <213> ORGANISM: Human

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171 <400> SEQUENCE: 4

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173 Met Met Tyr Ser Ala.Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe
174 1          5          10          15
177 Leu Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val
178          20          25          30
181 Asp Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val
182          35          40          45
185 Ser Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly
186          50          55          60
189 Lys His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp
190 65          70          75          80
193 Gly Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser
194          85          90          95
197 Gln Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn
198          100         105         110
201 Arg Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys
202          115         120         125
205 Val Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser
206          130         135         140
209 Ala Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro
210 145         150         155         160
213 Arg Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met
214          165         170         175
217 Lys Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr
218          180         185         190
221 Thr Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
222          195         200         205

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225 <210> SEQ ID NO: 5

226 <211> LENGTH: 2716

227 <212> TYPE: DNA

228 <213> ORGANISM: House Mouse

230 <400> SEQUENCE: 5

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233 tccgatgtgt tccgttacca gcgaccggca gcctgccatc gcagccccag tctgggtggg      120
235 gatcggagac aagtcccctg cagcagcggc aggcaagggt atataggaag agaaagagcc      180
237 aggcagcgcc agaggggaacg aacgagccga gcgaggaagg gagagccgag cgcaaggagg      240
239 agcgcacacg cacacacccg cgcgtaccg ctcgcgcaca gacagcgcg ggacagctca      300
241 caagtcctca ggttccgcgg acgagatgct gctgctgctg gccagatgtt ttctgggtgat      360
243 ccttgcttcc tcgctgctgg tgtgccccgg gctggcctgt gggcccggca gggggtttgg      420
245 aaagaggcgg caccccaata agctgacccc tttagcctac aagcagttta ttcccaacgt      480
247 agccgagaag accctagggg ccagcggcag atatgaaggg aagatcacia gaaactccga      540
249 acgatttaag gaactcacc ccaattacaa ccccgacatc atatttaagg atgaggaaaa      600
251 cacgggagca gaccggctga tgactcagag gtgcaaagac aagttaaatg ccttggccat      660
253 ctctgtgatg aaccagtggc ctggagtga gctgcgagt accgagggtt gggatgagga      720
255 cggccatcat tcagaggagt ctctacacta tgagggtcga gcagtggaca tcaccacgtc      780
257 cgaccgggac cgcagcaagt acggcatgct ggctcgccct gctgtggaag caggtttcga      840
259 ctgggtctac tatgaatcca aagctcacat ccactgttct gtgaaagcag agaactccgt      900
261 ggcggccaaa tccggcggtt gtttcccggg atccgccacc gtgcacctgg agcagggcgg      960
263 caccaagctg gtgaaggact tacgtcccgg agaccgcgtg ctggcggctg acgaccaggg      1020

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265 ccggctgctg tacagcgact tcctcacctt cctggaccgc gacgaaggcg ccaagaaggt 1080
267 cttctacgtg atcgagacgc tggagccgcg cgagcgctg ctgctcaccg ccgcgcacct 1140
269 gctcttcgtg gcgccgcaca acgactcggg gccacgccc gggccaagcg cgctctttgc 1200
271 cagccgcgtg cgcgccgggc agcgcgtgta cgtgggtggc gaacgcggcg gggaccgccg 1260
273 gctgctgccc gccgcggtgc acagcgtgac gctgcgagag gaggaggcg gcgcgtacgc 1320
275 gccgctcacg gcgcacggca ccattctcat caaccgggtg ctgcctcgt gctacgctgt 1380
277 catcgaggag cacagctggg cacaccgggc cttcgccct ttcgcctgg cgcacgcgt 1440
279 gctggccgcg ctggcaccgc cccgcacgga cggcgggggc gggggcagca tccctgcagc 1500
281 gcaatctgca acggaagcga ggggcgcgga gccgactgcg ggcattccact ggtactcgca 1560
283 gctgctctac cacattggca cctggctgtt ggacagcgag accatgcac ccttgggaat 1620
285 ggcggtcaag tccagctgaa gcccgacggg accgggcaag gggcgggagc ggcggggagc 1680
287 gactgcgaaa taaggaactg atgggaaagc gcacggaagg agacttttaa ttataagaat 1740
289 aattcataat aataataata atgataataa taataataat aagtagggca gtccaaagta 1800
291 gactataagg aagcaaaaac cccggggagt tctgttggtt tgtttagttt atatattttt 1860
293 ttttgaaatt tttcgttatt gtcttatatg ggttggtttt ctcctctcct ggctatttat 1920
295 ttgtttcgta tgaatagatg ttttaaaaat atgaacggac cttcaagagc cttactagt 1980
297 ttgtgtcttg gataatttat tattgtgtga actgtactca cagtgaggga aagattattt 2040
299 tctgaggcga agcaacctgc tgaaggtcta ttttctaca tctccttgt cctgcgtttc 2100
301 agaaggcaaa cctccgcatt cctctcctgc tatgctcctg ctttcccgca agtgtaaact 2160
303 aaaacctgct ccattgggggt ccacaaatta tatttttata cacagaattg taaattagat 2220
305 ttttgagaga tcaataccta actgaatgac atttcatttt ttgaaagtgt aaaatatgaa 2280
307 aatatattat ttttaatttaa ctattttcca atgtaatagc cgtcttctgt actgccttct 2340
309 tggtttgtat ttgctttgta accgccactt tgtcatgttc ttggaaacca agactgttaa 2400
311 cgcacacata tacacttttt tttttgacag actggaagaa ctctgttatt tttacttca 2460
313 aagaatttat tagaaaataa tattttttta aagtgcacct agcagcgagc ccacgaggat 2520
315 ggagcctgta gtttgtacag agaaaaacaa ggatgttttt gcattaataa actgagaagt 2580
317 aactgctgta aatttactaa aatgtatttt tgaatatatt gtaatagttt tatagaaata 2640
319 aagcgtgccca cacacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2700
321 aaaaaaaaaa aaaaaa 2716

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324 <210> SEQ ID NO: 6

325 <211> LENGTH: 437

326 <212> TYPE: PRT

327 <213> ORGANISM: House Mouse

329 <400> SEQUENCE: 6

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332 1 5 10 15
335 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
336 20 25 30
339 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Leu Gln Phe
340 35 40 45
343 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
344 50 55 60
347 Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
348 65 70 75 80
351 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
352 85 90 95
355 Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
356 100 105 110
359 Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly

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360	115	120	125
363	Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly		
364	130	135	140
367	Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly		
368	145	150	155
371	Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Trp		
372	165	170	175
375	Gly Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val		
376	180	185	190
379	Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu		
380	195	200	205
383	Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg		
384	210	215	220
387	Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu		
388	225	230	235
391	Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile		
392	245	250	255
395	Gly Thr Leu Glu Pro Arg Glu Pro Leu Leu Leu Thr Ala Ala His Leu		
396	260	265	270
399	Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser		
400	275	280	285
403	Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val		
404	290	295	300
407	Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser		
408	305	310	315
411	Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala		
412	325	330	335
415	His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val		
416	340	345	350
419	Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu		
420	355	360	365
423	Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly		
424	370	375	380
427	Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly		
428	385	390	395
431	Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His		
432	405	410	415
435	Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met		
436	420	425	430
439	Ala Val Lys Ser Ser		
440	435		

443 <210> SEQ ID NO: 7

444 <211> LENGTH: 3565

445 <212> TYPE: DNA

446 <213> ORGANISM: House Mouse

448 <400> SEQUENCE: 7

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451 cgcggcccg ggaggcggag acggagcacg gtgggcgccc agccgtcagt gcaggaggcc 120

453 gaggccgagc gggcggccgc gaggtagcag cgcgcggggc tgagggtacc tgaagctcag 180

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